

SCORE Search Results Details for Application 10529592 and Search Result 20090427_122913_us-10-529-592a-1.rge.

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This page gives you Search Results detail for the Application 10529592 and Search Result 20090427_122913_us-10-529-592a-1.rge.

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GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2009, 04:16:32 ; Search time 908 Seconds
(without alignments)
98090.438 Million cell updates/sec

Title: US-10-529-592A-1
Perfect score: 881
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14594359 seqs, 50548307366 residues

Total number of hits satisfying chosen parameters: 29188718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
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 16: gb_htg2:*
 17: gb_htg3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	881	100.0	881	2	CQ800176	CQ800176 Sequence
2	881	100.0	881	2	CS502806	CS502806 Sequence
3	881	100.0	881	2	DD295744	DD295744 GENES AND
4	827	93.9	893	2	CQ800178	CQ800178 Sequence
5	827	93.9	893	2	CS502808	CS502808 Sequence
6	827	93.9	893	2	DD295745	DD295745 GENES AND
c 7	611	69.4	614	2	DD131945	DD131945 Diagnosis
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c 9	611	69.4	614	2	EA064706	EA064706 Sequence
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c 11	549	62.3	211001	5	AC018695	AC018695 Homo sapi
c 12	547.4	62.1	160356	5	AC009068	AC009068 Homo sapi
c 13	542.6	61.6	189224	16	AC202720	AC202720 Pan trogl
14	433	49.1	447	2	CS539581	CS539581 Sequence
c 15	396.2	45.0	195676	16	AC198304	AC198304 Macaca mu
16	367	41.7	574	2	AX333084	AX333084 Sequence
17	367	41.7	574	2	DL064480	DL064480 Cancer Ge
18	261	29.6	229392	16	AC148906	AC148906 Otolemur
19	203	23.0	203	2	CQ716026	CQ716026 Sequence
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29	80.8	9.2	485	2	DL249991	DL249991 Organ-spe
c 30	75.4	8.6	763	2	DL022779	DL022779 Diagnosis
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ALIGNMENTS

RESULT 1

CQ800176

LOCUS CQ800176 881 bp DNA linear PAT 28-APR-2004

DEFINITION Sequence 1 from Patent WO2004031411.

ACCESSION CQ800176

VERSION CQ800176.1 GI:46849094

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura, Y. and Katagiri, T.

TITLE Genes and polypeptides relating to human pancreatic cancers

JOURNAL Patent: WO 2004031411-A 1 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The
President of the University of Tokyo (JP)

FEATURES

Location/Qualifiers

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/mol_type="unassigned DNA"
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CDS 163. .393

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ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;

Best Local Similarity 100.0%; Pred. No. 7.1e-254;

Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
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Qy	61	CGCCGCCGCCACCACCACGCGCCCGGGCGGGCTCGCGCGCTCGGGCGCGGCTCCGC	120
Db	61	CGCCGCCGCCACCACCACGCGCCCGGGCGGGCTCGCGCGCTCGGGCGCGGCTCCGC	120
Qy	121	AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	121	AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
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Qy	241	GTCTGAACGACAAGCACCTGGACGTGCCGACATCATCATCACGCCCCCACCACACG	300
Db	241	GTCTGAACGACAAGCACCTGGACGTGCCGACATCATCATCACGCCCCCACCACACG	300
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCTGTC	360
Db	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCTGTC	360
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
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Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCGCTCCGCTCAGAGAGACGTGGCAGG	540
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Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCAGGCCCCGCTGAGTG	600
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Qy 781 TGGAGTGGCTGTTTTTATAAGTTGTTTACAGATACGGAAACAGTCCAAAATGGGATT 840
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RESULT 2

CS502806

LOCUS CS502806 881 bp DNA linear PAT 02-APR-2007

DEFINITION Sequence 1 from Patent WO2007013358.

ACCESSION CS502806

VERSION CS502806.1 GI:138982984

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE

1
 AUTHORS Nakamura,Y., Katagiri,T. and Inaki,K.
 TITLE Vivit polypeptides, therapeutic agent comprising the same, and
 method of screening for anti-cancer agent
 JOURNAL Patent: WO 2007013358-A 1 01-FEB-2007;
 The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)

FEATURES

Location/Qualifiers
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 CDS 163. .393
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ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;
 Best Local Similarity 100.0%; Pred. No. 7.1e-254;
 Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCATGACCCCCGCTGTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC 60

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Qy      121 AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180

Qy      181 TGCTGAAAGGCTTTCAAATGTGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 240
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Qy      241 GTCCTGAACGACAAGCACCTGGACGTGCCGACATCATCATCACGCCCCCACCACCAG 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      301 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 360
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Qy 781 TGGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATT 840
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 Db 841 ATAATTTCTTTTTGCATTATAAAATAAAGATCCTCTGTAAC 881

RESULT 3

DD295744

LOCUS DD295744 881 bp DNA linear PAT 16-AUG-2006

DEFINITION GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS.

ACCESSION DD295744

VERSION DD295744.1 GI:112721854

KEYWORDS JP 2006500947-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 881)

AUTHORS Nakamura,Y. and Katagiri,T.

TITLE GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS

JOURNAL Patent: JP 2006500947-A 1 12-JAN-2006;
 ONCOTHERAPY SCIENCE INC, JAPAN AS REPRESENTED BY THE PRESIDENT OF
 THE UNIVERSITY OF TOKYO

COMMENT OS Homo sapiens

PN JP 2006500947-A/1

PD 12-JAN-2006

PF 12-SEP-2003 JP 2004541224

PR 30-SEP-2002 US 60/414872,28-FEB-2003 US 60/450889 PI

yusuke nakamura,toyomasa katagiri

CC

FH Key Location/Qualifiers

FT CDS (163)..(390).

FEATURES Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 881; DB 2; Length 881;
 Best Local Similarity 100.0%; Pred. No. 7.1e-254;
 Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGCCGAGCCCGAC 60
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Db 1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGCCGAGCCCGAC 60

Db 781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATT 840

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Db 841 ATAATTTCTTTTTTGCAATTATAAATAAAGATCCTCTGTAAC 881

RESULT 4

CQ800178

LOCUS CQ800178 893 bp DNA linear PAT 28-APR-2004

DEFINITION Sequence 3 from Patent WO2004031411.

ACCESSION CQ800178

VERSION CQ800178.1 GI:46849096

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y. and Katagiri,T.

TITLE Genes and polypeptides relating to human pancreatic cancers

JOURNAL Patent: WO 2004031411-A 3 15-APR-2004;

Oncotherapy Science, Inc. (JP); Japan as represented by The
 President of the University of Tokyo (JP)

FEATURES Location/Qualifiers

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CDS 197. .259

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Best Local Similarity 97.5%; Pred. No. 1.4e-237;

Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

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Qy 61 CGCCGCCGCCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 120
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Qy	181	TGCCTGAAAGGCTTTCAATGTGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
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Db	313	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	372
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	420
Db	373	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG	432
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	433	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	492
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACC CGGCTCCGCTCAGAGAGACGTGGCAGG	540
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Qy	661	TGGTCTGGCTGTTGGGGTCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720
Db	673	TGGTCTGGCTGTTGGGGTCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	732
Qy	721	CCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
Db	733	CCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	792
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Db	853	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	893

RESULT 5
 CS502808
 LOCUS CS502808 893 bp DNA linear PAT 02-APR-2007
 DEFINITION Sequence 3 from Patent WO2007013358.
 ACCESSION CS502808
 VERSION CS502808.1 GI:138982991
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Nakamura,Y., Katagiri,T. and Inaki,K.
 TITLE Vivit polypeptides, therapeutic agent comprising the same, and
 method of screening for anti-cancer agent
 JOURNAL Patent: WO 2007013358-A 3 01-FEB-2007;
 The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
 FEATURES
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 ORIGIN
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 Best Local Similarity 97.5%; Pred. No. 1.4e-237;
 Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;
 Qy 1 GGGCCATGACCCCCGCTGCTCTGTCTTGACAGGCTCGTCGCCGCGGGCCCCCGAGCCCGAC 60
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 Qy 181 TGCTGAAAGGCTTTCAATGTGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 240

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		TGCCTGAA-----AGCAGCAGCAGCAGCCACGACGAGGCCCCC		
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG	300	
Db	253			312
		GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG		
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360	
Db	313			372
		GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC		
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGCTCGGTTTGGCTGGCTGG	420	
Db	373			432
		CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGCTCGGTTTGGCTGGCTGG		
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	480	
Db	433			492
		CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG		
Qy	481	CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG	540	
Db	493			552
		CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG		
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCACAGGCCCCGCTGAGTG	600	
Db	553			612
		ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCACAGGCCCCGCTGAGTG		
Qy	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	660	
Db	613			672
		GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA		
Qy	661	TGGTCCTGGCTGTTGGGGTCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720	
Db	673			732
		TGGTCCTGGCTGTTGGGGTCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG		
Qy	721	CCCCCAGGGCTGTGCAAAACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780	
Db	733			792
		CCCCCAGGGCTGTGCAAAACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG		
Qy	781	TGGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT	840	
Db	793			852
		TGGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT		
Qy	841	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	881	
Db	853			893
		ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC		

RESULT 6

DD295745

LOCUS

DD295745

893 bp

DNA

linear

PAT 16-AUG-2006

DEFINITION GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS.
 ACCESSION DD295745
 VERSION DD295745.1 GI:112721855
 KEYWORDS JP 2006500947-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 893)
 AUTHORS Nakamura,Y. and Katagiri,T.
 TITLE GENES AND POLYPEPTIDES RELATING TO HUMAN PANCREATIC CANCERS
 JOURNAL Patent: JP 2006500947-A 2 12-JAN-2006;
 ONCOTHERAPY SCIENCE INC, JAPAN AS REPRESENTED BY THE PRESIDENT OF
 THE UNIVERSITY OF TOKYO
 COMMENT OS Homo sapiens
 PN JP 2006500947-A/2
 PD 12-JAN-2006
 PF 12-SEP-2003 JP 2004541224
 PR 30-SEP-2002 US 60/414872,28-FEB-2003 US 60/450889 PI
 yusuke nakamura,toyomasa katagiri
 CC
 FH Key Location/Qualifiers
 FT CDS (197)..(256).
 FEATURES Location/Qualifiers
 source 1..893
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 93.9%; Score 827; DB 2; Length 893;
 Best Local Similarity 97.5%; Pred. No. 1.4e-237;
 Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

Qy	1	GGGCCATGACCCCCGCTGCTCTGTCTTGCAAGGCTCGTCGCCGCGGCCCGCCCGAGCCCGAC	60
Db	35	GGGCCATGACCCCCGCTGCTCTGTCTTGCAAGGCTCGTCGCCGCGGCCCGCCCGAGCCCGAC	94
Qy	61	CGCCGCGGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	95	CGCCGCGGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	154
Qy	121	AGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	155	AGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	214
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	215	TGCCTGAA-----AGCAGCAGCAGCAGCCACGACGAGGCCCCC	252

Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCGACATCATCATCACGCCCCCACCACCCACG	300
Db	253	GTCCTGAACGACAAGCACCTGGACGTGCCGACATCATCATCACGCCCCCACCACCCACG	312
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	313	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	372
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG	420
Db	373	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG	432
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	433	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTG	492
Qy	481	CTGAATACCTGGATGGGAACTGAGCGAACCCGGGCGCTCCGCTCAGAGAGACGTGGCAGG	540
Db	493	CTGAATACCTGGATGGGAACTGAGCGAACCCGGGCGCTCCGCTCAGAGAGACGTGGCAGG	552
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCACAGGCCCCGCTGAGTG	600
Db	553	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCACAGGCCCCGCTGAGTG	612
Qy	601	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	660
Db	613	GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA	672
Qy	661	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	720
Db	673	TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG	732
Qy	721	CCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	780
Db	733	CCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG	792
Qy	781	TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT	840
Db	793	TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT	852
Qy	841	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	881
Db	853	ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	893

RESULT 7
DD131945/c

LOCUS	DD131945	614 bp	DNA	linear	PAT 04-NOV-2005
DEFINITION	Diagnosis and Prognosis of Breast Cancer Patients.				
ACCESSION	DD131945				

VERSION DD131945.1 GI:92825448
 KEYWORDS JP 2005500832-A/2531.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 614)
 AUTHORS Bernards,R., Vijver,M.J.V.D., Veer,L.J.V., Roberts,C.J., Mao,M.,
 Linsley,P.S., He,Y., Dai,H. and Hart,A.A.M.
 TITLE Diagnosis and Prognosis of Breast Cancer Patients
 JOURNAL Patent: JP 2005500832-A 2531 13-JAN-2005;
 Rosetta Inpharmatics
 COMMENT OS Homo sapiens
 PN JP 2005500832-A/2531
 PD 13-JAN-2005
 PF 14-JUN-2002 JP 2003505588
 PR 18-JUN-2001 US 60/298918,14-MAY-2002 US 60/380710 PI
 rene bernards,marc j van de vijver,laura johanna van't veer, PI
 christopher j roberts,mao mao,peter s linsley,yudong he, PI
 hongyue dai,
 PI a a m hart
 CC
 FH Key Location/Qualifiers.
 FEATURES Location/Qualifiers
 source 1..614
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 69.4%; Score 611; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 2.2e-172;
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 271 GACATCATCATCACGCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 330
 Db 614 GACATCATCATCACGCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 555
 Qy 331 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCC 390
 Db 554 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCC 495
 Qy 391 TGAGGAGGTGTCTCTGGGTTTGGCTGGCTGGCTCTGTCTCCAGCGGCCCGGCTTCAGGTGT 450
 Db 494 TGAGGAGGTGTCTCTGGGTTTGGCTGGCTGGCTCTGTCTCCAGCGGCCCGGCTTCAGGTGT 435
 Qy 451 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAAC 510
 Db 434 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAAC 375

Qy 511 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 570
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 Db 374 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 315

Qy 571 AGAACAGTGTTCCTCCAGGCCCCGCTGAGTGGACCGACCTCTGACACCTCCAGGTTCTTG 630
 |||
 Db 314 AGAACAGTGTTCCTCCAGGCCCCGCTGAGTGGACCGACCTCTGACACCTCCAGGTTCTTG 255

Qy 631 CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTTGCTGTGGGGTCCCAGGGAGAG 690
 |||
 Db 254 CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTTGCTGTGGGGTCCCAGGGAGAG 195

Qy 691 GCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAAACATGCCCTTG 750
 |||
 Db 194 GCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAAACATGCCCTTG 135

Qy 751 CCATAAGCACCAACAAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTATAAGTTGTTTTA 810
 |||
 Db 134 CCATAAGCACCAACAAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTATAAGTTGTTTTA 75

Qy 811 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCAATTATAAATAAAGA 870
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 Db 74 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCAATTATAAATAAAGA 15

Qy 871 TCCTCTGTAAC 881
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 Db 14 TCCTCTGTAAC 4

RESULT 8

DD417196/c

LOCUS DD417196 614 bp DNA linear PAT 26-MAR-2007

DEFINITION Diagnosis and Prognosis of Breast Cancer Patients.

ACCESSION DD417196

VERSION DD417196.1 GI:134130622

KEYWORDS JP 2006519591-A/2531.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 614)

AUTHORS He, Y. and Veer, L.J.V.

TITLE Diagnosis and Prognosis of Breast Cancer Patients

JOURNAL Patent: JP 2006519591-A 2531 31-AUG-2006;

Rosetta Inpharmatics LLC JUERGEN HERMANN NETT

COMMENT OS Homo sapiens

PN JP 2006519591-A/2531

PD 31-AUG-2006

PF 15-JAN-2004 JP 2006500977

PR 15-JAN-2003 US 10/342887
 PI yudong he,laura johanna van't veer
 CC
 FH Key Location/Qualifiers.

FEATURES
 source 1. .614
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 69.4%; Score 611; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 2.2e-172;
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	271	GACATCATCATCACGCCCCCACCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC	330
Db	614	GACATCATCATCACGCCCCCACCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC	555
Qy	331	ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	390
Db	554	ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	495
Qy	391	TGAGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT	450
Db	494	TGAGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT	435
Qy	451	CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAAC	510
Db	434	CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAAC	375
Qy	511	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	570
Db	374	CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC	315
Qy	571	AGAACAGTGTTTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	630
Db	314	AGAACAGTGTTTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG	255
Qy	631	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAG	690
Db	254	CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAG	195
Qy	691	GCTCTCTTCTGGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACATGCCCTTG	750
Db	194	GCTCTCTTCTGGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACATGCCCTTG	135
Qy	751	CCATAAGCACCAACAAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTATAAGTTGTTTTA	810
Db	134	CCATAAGCACCAACAAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTATAAGTTGTTTTA	75

QY 811 CAGATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTGCATTATAAATAAGA 870
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 Db 74 CAGATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTGCATTATAAATAAGA 15

QY 871 TCCTCTGTAAC 881
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 Db 14 TCCTCTGTAAC 4

RESULT 9

EA064706/c

LOCUS EA064706 614 bp DNA linear PAT 07-FEB-2007

DEFINITION Sequence 2531 from patent US 7171311.

ACCESSION EA064706

VERSION EA064706.1 GI:125176216

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 614)

AUTHORS Dai,H., He,Y., Linsley,P.S., Mao,M., Roberts,C.J., Van't Veer,L.J.,
 Van de Vijver,M.J., Bernards,R. and Hart,A.A.M.

TITLE Methods of assigning treatment to breast cancer patients

JOURNAL Patent: US 7171311-A 2531 30-JAN-2007;
 Rosetta Inpharmatics LLC and Netherlands Cancer Institute; Seattle,
 WA;
 US;

FEATURES Location/Qualifiers

source 1. .614
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 69.4%; Score 611; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 2.2e-172;
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GACATCATCATCACGCCCCCACCACGCGGCATGATGCTGCCGAGGGACTTGGGGAGC 330
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 Db 614 GACATCATCATCACGCCCCCACCACGCGGCATGATGCTGCCGAGGGACTTGGGGAGC 555

QY 331 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 390
 |||
 Db 554 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 495

QY 391 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 450
 |||
 Db 494 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 435

QY 451 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTTGGATGGGAACCTGAGCGAAC 510

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Db      434 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACAGAGCAAC 375
      |||
Qy      511 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 570
      |||
Db      374 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 315
      |||
Qy      571 AGAACAGTGTTTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG 630
      |||
Db      314 AGAACAGTGTTTCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG 255
      |||
Qy      631 CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTGGGGTCCCAGGGAGAG 690
      |||
Db      254 CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTGGGGTCCCAGGGAGAG 195
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Qy      691 GCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTG 750
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Db      194 GCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTG 135
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Qy      751 CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTA 810
      |||
Db      134 CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTA 75
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Qy      811 CAGATACGGAACAGTCCAAAATGGGATTATTAATTTCTTTTTTGCAATTATAAATAAAGA 870
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Db      74 CAGATACGGAACAGTCCAAAATGGGATTATTAATTTCTTTTTTGCAATTATAAATAAAGA 15
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Qy      871 TCCTCTGTAAC 881
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Db      14 TCCTCTGTAAC 4

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RESULT 10
AC123908/c

LOCUS AC123908 185321 bp DNA linear PRI 28-MAR-2003
 DEFINITION Homo sapiens chromosome 16 clone CTD-2542L18, complete sequence.
 ACCESSION AC123908
 VERSION AC123908.3 GI:29336199
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 185321)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
 Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 185321)

AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 185321)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (06-SEP-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 185321)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Mar 28, 2003 this sequence version replaced gi:22748376.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.1.

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 1. .185321
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="CTD-2542L18"

ORIGIN

Query Match 62.3%; Score 549; DB 5; Length 185321;
 Best Local Similarity 100.0%; Pred. No. 1.2e-153;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 333 AGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db 124973 AGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTG 124914

Qy 393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
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Db 124913 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 124854

Qy 453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAACCC 512
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Db 124853 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGCGAACCC 124794

Qy 513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
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Db 124793 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 124734

Qy 573 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
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 Db 124733 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 124674

Qy 633 GACTCCGGCCTGGTGAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
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 Db 124673 GACTCCGGCCTGGTGAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 124614

Qy 693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAACACATGCCCTGCC 752
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 Db 124613 TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAACACATGCCCTGCC 124554

Qy 753 ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 812
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 Db 124553 ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 124494

Qy 813 GATACGGAAACAGTCCAAAATGGGATTATAAATTTCTTTTTTGCAATTATAAATAAGATC 872
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Qy 873 CTCTGTAAC 881
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RESULT 11
 AC018695/c

LOCUS AC018695 211001 bp DNA linear PRI 09-JAN-2002
 DEFINITION Homo sapiens BAC clone RP11-568J23 from 16, complete sequence.
 ACCESSION AC018695
 VERSION AC018695.6 GI:13443271
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 211001)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 PUBMED 9847074

REFERENCE 2 (bases 1 to 211001)
 AUTHORS Haakenson, W., Scott, K., Courtney, L., Drone, K., Gregory, S. and Lesley, K.
 TITLE The sequence of Homo sapiens BAC clone RP11-568J23
 JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 211001)
 AUTHORS Waterston, R.H.

TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 211001)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 211001)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 6 (bases 1 to 211001)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Mar 24, 2001 this sequence version replaced gi:9838280.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0568J23

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-542M13. Actual start of this clone is at base position 1 of RP11-568J23; actual end is at base position 211001 of RP11-568J23.

H_NH0568J23 contains an imperfect GA run from 143896 to 144293, in which the exact length is unknown. There are approximately 800 bases missing according to the restriction digests and pcr data.

H_NH0568J23 contains a single stranded region from 144079 to 144172 which contains low quality data.

FEATURES	Location/Qualifiers
source	1. .211001 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="16" /map="16" /clone="RP11-568J23" /clone_lib="RPCI-11"
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repeat_region	407. .467 /rpt_family="MIR"
repeat_region	760. .835 /rpt_family="MIR"
repeat_region	891. .929 /rpt_family="MER1_type"
repeat_region	939. .1114 /rpt_family="L1"
repeat_region	1115. .1254 /rpt_family="Alu"
repeat_region	1255. .1555 /rpt_family="Alu"
repeat_region	1530. .1555 /rpt_family="(A)n"
repeat_region	1556. .1723 /rpt_family="Alu"
repeat_region	1724. .2020 /rpt_family="L1"
repeat_region	2023. .2332 /rpt_family="Alu"

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repeat_region      3022. .3340
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repeat_region      3024. .3051
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Query Match 62.3%; Score 549; DB 5; Length 211001;
 Best Local Similarity 100.0%; Pred. No. 1.2e-153;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      333 AGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db      17960 AGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTG 17901

Qy      393 AGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
          |||
Db      17900 AGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 17841

Qy      453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACCTGAGCGAACCC 512
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Qy      513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
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Db      17780 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 17721

Qy      573 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
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Db      17720 AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 17661

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Qy      633  GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
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Qy      693  TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAAACACATGCCCTTGCC 752
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Db      17600 TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAAACACATGCCCTTGCC 17541

Qy      753  ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACA 812
          |||
Db      17540 ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACA 17481

Qy      813  GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAATAAGATC 872
          |||
Db      17480 GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAATAAGATC 17421

Qy      873  CTCTGTAAC 881
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Db      17420 CTCTGTAAC 17412
    
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RESULT 12
AC009068/c

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LOCUS      AC009068                      160356 bp      DNA      linear      PRI 27-APR-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-314K3, complete sequence.
ACCESSION  AC009068
VERSION    AC009068.10  GI:13811892
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
            ORGANISM  Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 160356)
            AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
            TITLE      Direct Submission
            JOURNAL     Unpublished
REFERENCE  2 (bases 1 to 160356)
            AUTHORS   DOE Joint Genome Institute.
            TITLE      Direct Submission
            JOURNAL     Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
                Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE  3 (bases 1 to 160356)
            AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
            TITLE      Direct Submission
            JOURNAL     Submitted (27-APR-2001) DOE Joint Genome Institute, 2800 Mitchell
                Drive, Walnut Creek, CA 94598, USA
COMMENT    On Apr 27, 2001 this sequence version replaced gi:12000278.
FEATURES   Location/Qualifiers
            source     1. .160356
    
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-314K3"
misc_feature 1. .160356
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Institute;
www.jgi.doe.gov;
Finishing Completed at Stanford Human Genome Center;
www-shgc.stanford.edu;
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.3.;
STS Content;;
WI-11796 G24048;
SHGC-37143 G30481"

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ORIGIN

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Query Match          62.1%; Score 547.4; DB 5; Length 160356;
Best Local Similarity 99.8%; Pred. No. 3.6e-153;
Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      333 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 392
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Db      79810 AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG 79751

Qy      393 AGGAGGTGTCTCGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
      |||
Db      79750 AGGAGGTGTCTCGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 79691

Qy      453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC 512
      |||
Db      79690 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC 79631

Qy      513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
      |||
Db      79630 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 79571

Qy      573 AACAGTGTTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
      |||
Db      79570 AACAGTGTTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 79511

Qy      633 GACTCCGGCCTGGTGAAGGGAGCGCCATGGTCTTGGCTGTTGGGGTCCCAGGGAGAGGC 692
      |||
Db      79510 GACTCCGGCCTGGTGAAGGGAGCGCCATGGTCTTGGCTGTTGGGGTCCCAGGGAGAGGC 79451

Qy      693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCC 752
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Db      79450 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCC 79391

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Qy 753 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 812
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Qy 813 GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
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 Db 79330 GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCATTATAAATAAAGATC 79271

Qy 873 CTCTGTAAC 881
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 Db 79270 CTCTGTAAC 79262

RESULT 13
 AC202720/c

LOCUS AC202720 189224 bp DNA linear HTG 29-MAY-2008
 DEFINITION Pan troglodytes chromosome 16 clone CH251-467D6, WORKING DRAFT
 SEQUENCE.

ACCESSION AC202720
 VERSION AC202720.2 GI:189163682
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 189224)
 AUTHORS Wilson,R.K.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-2007) Genetics, Genome Sequencing Center, 4444
 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 2 (bases 1 to 189224)
 AUTHORS Wilson,R.K.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-2008) Genetics, Genome Sequencing Center, 4444
 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On May 29, 2008 this sequence version replaced gi:145587712.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site:http://genome.wustl.edu
 Contact: submissions@watson.wustl.edu
 ----- Project Information -----
 Center project name: C_AB0467D06

----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319
 Consensus quality: 188692 bases at least Q40
 Consensus quality: 188913 bases at least Q30
 Consensus quality: 189064 bases at least Q20

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 189224: contig of 189224 bp in length.

FEATURES

source

Location/Qualifiers

1. .189224
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /chromosome="16"
 /clone="CH251-467D6"

misc_feature

1. .189224
 /note="assembly_name:Contig5;
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 vector_side:right"

ORIGIN

Query Match 61.6%; Score 542.6; DB 16; Length 189224;
 Best Local Similarity 99.3%; Pred. No. 1e-151;
 Matches 545; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
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Qy	393	AGGAGGTGTCTCGGTTTGGCTGGCTGGCTCCTGCTCCAGCGCCCGGCTTCAGGTGTCC	452
Db	116533	AGGAGGTGTCTCGGTTTGGCTGGCTGGCTCCTGCTCCAGCGCCCGGCTTCAGGTGTCC	116474
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAAGTGGGAACTGAGCGAACCC	512
Db	116473	GGGGGTGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAAGTGGGAACTGAGCGAATCC	116414
Qy	513	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	572
Db	116413	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCAAGGAATCCAGCCTGCCACTTCCAG	116354
Qy	573	AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	116353	AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	116294

Qy 633 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
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 Db 116293 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 116234

Qy 693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAAACACATGCCCTTGCC 752
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Qy 753 ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACA 812
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Qy 873 CTCTGTAAC 881
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 Db 116053 CTCTGTAAC 116045

RESULT 14

CS539581

LOCUS CS539581 447 bp DNA linear PAT 20-APR-2007

DEFINITION Sequence 168 from Patent WO2007012811.

ACCESSION CS539581

VERSION CS539581.1 GI:145584734

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Maitland, N. and Bryce, S.

TITLE Stem cell markers

JOURNAL Patent: WO 2007012811-A 168 01-FEB-2007;

Procure Therapeutics Limited (GB)

FEATURES Location/Qualifiers

source 1. .447

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 49.1%; Score 433; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 1.2e-118;

Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      15  GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGGCCCCCGAGCCCGAC  74
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Db      75  CGCCGCCGCCACCACCACCAGCGCCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC  134
Qy     121  AGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC  180
Db     135  AGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC  194
Qy     181  TGCCTGAAAGGCTTTCAAATGTGTGTACGAGCAGCAGCAGCAGCCACGACGAGGCCCCCC  240
Db     195  TGCCTGAAAGGCTTTCAAATGTGTGTACGAGCAGCAGCAGCAGCCACGACGAGGCCCCCC  254
Qy     241  GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG  300
Db     255  GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG  314
Qy     301  GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC  360
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Qy     361  CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGCTCTGGGTTTGGCTGGCTGG  420
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Qy     421  CTCCTGCTCCAGC  433
Db     435  CTCCTGCTCCAGC  447

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RESULT 15
AC198304/c

LOCUS AC198304 195676 bp DNA linear HTG 14-APR-2007

DEFINITION Macaca mulatta clone CH250-65C9, WORKING DRAFT SEQUENCE, 4 ordered pieces.

ACCESSION AC198304

VERSION AC198304.4 GI:145279267

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 195676)

AUTHORS Muzny,D.M., Abraham,K.K., Abulimiti,A., Adams,C.Q., Aduba,G., Allen,C.C., Alsbrooks,S.L., Anosike,U.S., Archer,P.M., Arredondo,H.H., Attaway,T., Bandaranaike,D.P., Bangura,L., Barton,S.R., Bell,A.V., Bell,S.N., Beraducci,A.R., Bickham,C.,

Biswal, K., Blyth, P.R., Buhay, C.J., Canada, A., Cardenas, V.,
 Carter, K., Chacko, J., Chandrabose, M.N., Chavez, A., Chavez, D.,
 Chen, G., Chen, R., Chu, H., Clerc blankenburg, K.P., Cockrell, R.,
 Cooper, J.A., Coyle, M.D., Cree, A., Cueto, C.B., Curry, S.M., Dai, W.,
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 Gonzalez-Garay, M.L., Guevara, W.V., Haaland, W.C., Haeberlen, K.A.,
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 Kowis, A.N., Kowis, C.R., Lago, L.A., Lago, M.T., Lai, C., Lara, F.,
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 Lewis, L.R., Li, B., Li, Y., Li, Z., Linnell, M.A., Liu, J., Liu, W.,
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 Lozado, R.J., Luc, T., Madu, R.C., Maheshwari, M., Maheshwari, R.,
 Malloy, K., Mansouri, D.L., Martinez, E., Matejkova, P., Mathew, T.,
 Mccauley, S.K., Mcpherson, J.D., Mercado, C., Mercado, I.C.,
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 Nguyen, H.T., Nguyen, N.B., Nguyen, P.Q., Nwaokemele, O.O.,
 Obregon, M., Odeh, E.A., Okonkwo, F., Okwuonu, G.O., Okwuonu, K.C.,
 Onyenekwe, J., Parish, B.J., Parker, D.N., Parra, A.A., Pasternak, S.,
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 Perez, Y.Y., Pham, T.L., Player, E.J., Primus, E.L., Pu, L., Puazo, M.,
 Purkiss, C., Qin, X., Quiroz, J.B., Rabata, D., Rachlin, E.K., Ren, Y.,
 Richards, S., Rojas, A., Ruiz, S., Sabo, A., Santibanez, J.,
 Savery, G.G., Scherer, S.E., Schneider, B.W., Sebasigari, R.,
 Sexton, M.M., Shen, H., Shen, Y., Sisson, I., Sneed, A.J., Sodergren, E.,
 Song, X., Sorelle, R.P., Svatek, A.F., Taylor, E.W., Taylor, T.R.,
 Thelus, R., Thomas, N., Thorn, R.D., Thornton, R.D., Tong, M.Y.,
 Trejos, Z.Y., Usmani, K., Vargo, C.E., Vattathil, S., Vega, R.A.,
 Villasana, D., Volkov, A., Walker, D.L., Wang, Q., Wang, S.,
 Warren, J.T., Watt, J.E., Wei, X., Wheeler, D.A., White, C.S., Williams
 jr, R.L., Williams, A.C., Williams, G.A., Williams, J.D., Wilson, K.,
 Woodworth, J.R., Worley, K.C., Wright, R.A., Wu, J., Wu, W., Yakub, S.,
 Yerrapragada, S., Yu, F., Yuan, D.T., Yuan, Y., Zhang, J., Zhang, L.,
 Zhang, Z., Zhou, J., Zhu, Y., Weinstock, G. and Gibbs, R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 195676)

AUTHORS Worley, K.C.

TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2007) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 195676)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (14-APR-2007) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Apr 14, 2007 this sequence version replaced gi:133754372.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help.tmc.edu
 ----- Project Information
 Center project name: LEYX
 Center clone name: CH250-65C9
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 200531 bases at least Q40
 Consensus quality: 200802 bases at least Q30
 Consensus quality: 200989 bases at least Q20
 Estimated insert size: 206589; sum-of-contigs estimation
 Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * The sequence data in this record represents an 'enhanced' version
 * of a Phase 2 submission. The indicated order and orientation of
 * each sequence has been established using one or more of the
 * following: read-pair data from individual subclones, overlaps
 * with neighboring clones, alignment with available reference
 * sequence (e.g., human), and/or confirmation by PCR testing.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 142140: contig of 142140 bp in length
 * 142141 142840: gap of 700 bp
 * 142841 154919: contig of 12079 bp in length
 * 154920 155019: gap of 100 bp

* 155020 160424: contig of 5405 bp in length
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 * 161325 195676: contig of 34352 bp in length.

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 /note="assembly_name:Contig59"

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 Db 36045 AGTCTGGTGGATGAGACAGGGTCGTGCCGGATGATGGAGAACTCGACCCAGAAGCCTG 35986
 Qy 393 AGGAGGTGTCTGGGTTTGGCTGGCTGCTCCTGCTCCAGCGGCGCGGCTTCAGGTGTCC 452
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 Db 35985 AGGAGGTGTCTGGATTGTCTGGTGGGCTCCTGCTGCGGGGTCCCAGCTTCAGGTGTCC 35926
 Qy 453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTTGGATGGGAAGTGAAGCAACCC 512
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 Db 35925 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTTGGATGGGAAGTGAAGCAATCT 35866
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Qy	693	TCTCTTCTGGACAAACACACCCTCCCAGCCCCAGGGCTGTGCAAAACACATGCCCTTGCC	752
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Qy	753	ATAAGCACCAACAAGAAGTCTTTCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTT	809
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